```
    RAW SEQUENCE LISTING                      DATE: 09/16/2004
    PATENT APPLICATION:   US/09/940,673B      TIME: 11:44:05

    Input Set : A:\22311040.app
    Output Set: N:\CRF4\09162004\I940673B.raw
```

```
 3 <110> APPLICANT: GORSKI, DAVID H.
 4          WALSH, KENNETH
 6 <120> TITLE OF INVENTION: GROWTH ARREST HOMEOBOX GENE
 8 <130> FILE REFERENCE: 22311/04015
10 <140> CURRENT APPLICATION NUMBER: 09/940,673B
11 <141> CURRENT FILING DATE: 2001-08-27
13 <150> PRIOR APPLICATION NUMBER: 09/078,465
14 <151> PRIOR FILING DATE: 1998-05-14
16 <150> PRIOR APPLICATION NUMBER: 08/203,532
17 <151> PRIOR FILING DATE: 1994-02-24
19 <160> NUMBER OF SEQ ID NOS: 19
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 2244
25 <212> TYPE: DNA
26 <213> ORGANISM: Rattus sp.
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (197)..(1105)
32 <400> SEQUENCE: 1
33 gtcaagtgtt tatacgtgca ggagactggc cgctcggctc aggactggga ttagcgggct 60
35 ctgctcaaac ccgcgcggct tttacattag gagtgagtgg gggagagtcc taggatttct 120
37 agtgaaaagt gacagcgctt ggtggacttt gggaccttcg tgaagtcttc tgcttggaag 180
39 ctgagacttg catgcc atg gaa cac ccc ctc ttt ggc tgc ctg cgc agc ccc 232
40                     Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser Pro
41                      1               5                  10
43 cac gcc aca gcg caa ggc ttg cac ccc ttc tcg cag tct tct ctg gcc  280
44 His Ala Thr Ala Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu Ala
45          15                  20                  25
47 ctc cat gga aga tct gac cac atg tcc tac ccc gaa ctc tcc aca tct  328
48 Leu His Gly Arg Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr Ser
49      30                  35                  40
51 tcc tcg tct tgc ata atc gcg gga tac ccc aat gag gag ggc atg ttt  376
52 Ser Ser Ser Cys Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met Phe
53 45                  50                  55                  60
55 gcc agc cag cat cac agg ggg cac cac cac cac cac cac cac cac cat  424
56 Ala Ser Gln His His Arg Gly His His His His His His His His His
57                  65                  70                  75
59 cac cac cac cag cag cag cag cac cag gct ctg caa agc aac tgg cac  472
60 His His His Gln Gln Gln Gln His Gln Ala Leu Gln Ser Asn Trp His
61              80                  85                  90
63 ctc ccg cag atg tcc tcc ccg cca agc gcg gcc cgg cac agc ctt tgc  520
64 Leu Pro Gln Met Ser Ser Pro Pro Ser Ala Ala Arg His Ser Leu Cys
```

```
65          95                   100                  105
67 ctg cag cct gat tcc gga ggg ccc ccg gag ctg ggg agc agc cct ccg   568
68 Leu Gln Pro Asp Ser Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro Pro
69     110                  115                  120
71 gtc ctg tgc tcc aac tct tct agc ctg ggc tcc agc acc ccg acc gga   616
72 Val Leu Cys Ser Asn Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr Gly
73 125                  130                  135                  140
75 gcc gcg tgc gca cca agg gat tat ggc cgt caa gcg ctg tca ccc gca   664
76 Ala Ala Cys Ala Pro Arg Asp Tyr Gly Arg Gln Ala Leu Ser Pro Ala
77             145                  150                  155
79 gaa gtg gag aag aga agt ggc agc aaa aga aaa agc gac agt tca gat   712
80 Glu Val Glu Lys Arg Ser Gly Ser Lys Arg Lys Ser Asp Ser Ser Asp
81         160                  165                  170
83 tcc cag gaa gga aat tac aag tca gaa gtg aac agc aaa cct agg aag   760
84 Ser Gln Glu Gly Asn Tyr Lys Ser Glu Val Asn Ser Lys Pro Arg Lys
85         175                  180                  185
87 gaa aga aca gct ttc acc aaa gag caa atc aga gaa ctt gag gca gag   808
88 Glu Arg Thr Ala Phe Thr Lys Glu Gln Ile Arg Glu Leu Glu Ala Glu
89     190                  195                  200
91 ttc gcc cat cat aac tat ctg acc aga ctg aga aga tat gag ata gcg   856
92 Phe Ala His His Asn Tyr Leu Thr Arg Leu Arg Arg Tyr Glu Ile Ala
93 205                  210                  215                  220
95 gtg aac cta gac ctc act gaa aga cag gtg aaa gtg tgg ttc cag aac   904
96 Val Asn Leu Asp Leu Thr Glu Arg Gln Val Lys Val Trp Phe Gln Asn
97                  225                  230                  235
99 agg aga atg aag tgg aag cgg gtc aag ggg gga caa caa gga gct gca   952
100 Arg Arg Met Lys Trp Lys Arg Val Lys Gly Gly Gln Gln Gly Ala Ala
101             240                  245                  250
103 gcc cga gaa aag gaa ctg gtg aat gtg aaa aag gga aca ctt ctt cca   1000
104 Ala Arg Glu Lys Glu Leu Val Asn Val Lys Lys Gly Thr Leu Leu Pro
105     255                  260                  265
107 tca gag ctg tca gga att ggt gca gcc acc ctc cag cag aca ggg gac   1048
108 Ser Glu Leu Ser Gly Ile Gly Ala Ala Thr Leu Gln Gln Thr Gly Asp
109     270                  275                  280
111 tca cta gca aat gac gac agt cgc gat agt gac cac agc tct gag cac   1096
112 Ser Leu Ala Asn Asp Asp Ser Arg Asp Ser Asp His Ser Ser Glu His
113 285                  290                  295                  300
115 gca cac tta tgatacatac agagaccagc tccgttctca ggaaagcacc          1145
116 Ala His Leu
118 attgtgatgg caaatctcac ccaaacatcg tttacatggc agatgactgt ggcagtgttg 1205
120 cttaatataa ttaaacgcag gcatctcaag tctgtttctc atgattgata gaaggtttac 1265
122 actaagtgcc tcttattgaa gatgcttcca cagtgaaatt ggagaaagtg aacatatcta 1325
124 aatatacttg ttccttatat gacagagagg gagatgaatg tttgctttgg cttgcactga 1385
126 aaattaaatt gctaccaaga gcaaactcgg taagacattt tgactcaagt tgtctccaga 1445
128 gtgaagatgt tatagaaatg ctttgaacat tccagttgta ccaggtcatg tgtgtgacac 1505
130 tgggcaggta tttgctttTg cttgcactga aacttaaact gctatcaagt taacccatga 1565
132 aatagtttat cttgaacagc cacagtgcct gaaatcacca agtggatata aaatgaactg 1625
134 aaattctgta tatattactc ctaagtcatt ttcctgtctt cactaatttt agcaaatgca 1685
136 ttcatattag ctgatgaaaa taggctttcc cgtggacaaa tgcagccagc ttcttgtatt 1745
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/940,673B

DATE: 09/16/2004
TIME: 11:44:05

Input Set : A:\22311040.app
Output Set: N:\CRF4\09162004\I940673B.raw

```
138 tttatacatt tttttgtcag tcagagacat cagtatgtgc ttacttgtgt tcaagtagag 1805
140 gaaatgcagt agagtctgat aggacatatt cttggtacca cagacaaaac aaatcttctg 1865
142 ttgcattgac tatcaactgc tgcagataca ttagagaaca cacctagccc ccctccagcc 1925
144 tccctctgtt atcgctcgaa gacattagcg tcataggcaa gtagttacct tgccaaatga 1985
146 gtcttgtgtg gcagatgtct gattttgtat ctttaaactg ttaatggtat gtgtctgctt 2045
148 cagttaacag ggaaaaagat ttcttcctca ttgtttatga tacaaaaccc aagtgccaaa 2105
150 caaagctagt tcttcaaggg atagatgaga aactgaatgt ctgacaagta gactcagcga 2165
152 aaatacatta tttttcagag gctgtgtatt catgcagtac aagtccttgt attttgtaaa 2225
154 aaaaaaagtt aaataaatg                                                2244
```

157 <210> SEQ ID NO: 2
158 <211> LENGTH: 303
159 <212> TYPE: PRT
160 <213> ORGANISM: Rattus sp.

162 <400> SEQUENCE: 2
```
163 Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser Pro His Ala Thr Ala
164  1               5                  10                  15
166 Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu Ala Leu His Gly Arg
167              20                  25                  30
169 Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr Ser Ser Ser Ser Cys
170          35                  40                  45
172 Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met Phe Ala Ser Gln His
173          50                  55                  60
175 His Arg Gly His His His His His His His His His His His His Gln
176  65                  70                  75                  80
178 Gln Gln Gln His Gln Ala Leu Gln Ser Asn Trp His Leu Pro Gln Met
179              85                  90                  95
181 Ser Ser Pro Pro Ser Ala Ala Arg His Ser Leu Cys Leu Gln Pro Asp
182             100                 105                 110
184 Ser Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro Pro Val Leu Cys Ser
185             115                 120                 125
187 Asn Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr Gly Ala Ala Cys Ala
188         130                 135                 140
190 Pro Arg Asp Tyr Gly Arg Gln Ala Leu Ser Pro Ala Glu Val Glu Lys
191 145                 150                 155                 160
193 Arg Ser Gly Ser Lys Arg Lys Ser Asp Ser Ser Asp Ser Gln Glu Gly
194             165                 170                 175
196 Asn Tyr Lys Ser Glu Val Asn Ser Lys Pro Arg Lys Glu Arg Thr Ala
197         180                 185                 190
199 Phe Thr Lys Glu Gln Ile Arg Glu Leu Glu Ala Glu Phe Ala His His
200         195                 200                 205
202 Asn Tyr Leu Thr Arg Leu Arg Arg Tyr Glu Ile Ala Val Asn Leu Asp
203     210                 215                 220
205 Leu Thr Glu Arg Gln Val Lys Val Trp Phe Gln Asn Arg Arg Met Lys
206 225                 230                 235                 240
208 Trp Lys Arg Val Lys Gly Gly Gln Gln Gly Ala Ala Ala Arg Glu Lys
209             245                 250                 255
211 Glu Leu Val Asn Val Lys Lys Gly Thr Leu Leu Pro Ser Glu Leu Ser
212             260                 265                 270
214 Gly Ile Gly Ala Ala Thr Leu Gln Gln Thr Gly Asp Ser Leu Ala Asn
```

```
215            275              280                 285
217 Asp Asp Ser Arg Asp Ser Asp His Ser Ser Glu His Ala His Leu
218       290                295                300
222 <210> SEQ ID NO: 3
223 <211> LENGTH: 941
224 <212> TYPE: DNA
225 <213> ORGANISM: Homo sapiens
227 <220> FEATURE:
228 <221> NAME/KEY: CDS
229 <222> LOCATION: (33)..(938)
231 <400> SEQUENCE: 3
232 gtcttctacc tggaacccga aacttgcatg ct atg gaa cac ccg ctc ttt ggc    53
233                                    Met Glu His Pro Leu Phe Gly
234                                     1               5
236 tgc ctg cgc agc cct cac gcc acg gcg caa ggc ttg cac ccg ttc tcc   101
237 Cys Leu Arg Ser Pro His Ala Thr Ala Gln Gly Leu His Pro Phe Ser
238           10              15                  20
240 caa tcc tct ctc gcc ctc cat gga aga tct gac cat atg tct tac ccc   149
241 Gln Ser Ser Leu Ala Leu His Gly Arg Ser Asp His Met Ser Tyr Pro
242       25              30                  35
244 gag ctc tct act tct tcc tca tct tgc ata atc gcg gga tac ccc aac   197
245 Glu Leu Ser Thr Ser Ser Ser Ser Cys Ile Ile Ala Gly Tyr Pro Asn
246   40              45              50                  55
248 gaa gag gac atg ttt gcc agc cag cat cac agg ggg cac cac cac cac   245
249 Glu Glu Asp Met Phe Ala Ser Gln His His Arg Gly His His His His
250           60              65                  70
252 cac cac cac cat cac cac cat cag cag cag cag cac cag gct ctg caa   293
253 His His His His His His His Gln Gln Gln Gln His Gln Ala Leu Gln
254           75              80                  85
256 acc aac tgg cac ctc ccg cag atg tct tcc cca ccg agt gcg gct cgg   341
257 Thr Asn Trp His Leu Pro Gln Met Ser Ser Pro Pro Ser Ala Ala Arg
258           90              95                  100
260 cat agc ctc tgc ctc cag ccc gac tct gga ggg ccc cca gag ttg ggg   389
261 His Ser Leu Cys Leu Gln Pro Asp Ser Gly Gly Pro Pro Glu Leu Gly
262       105             110                 115
264 agc agc ccg ccc gtc ctg tgc tcc aac tct tcc agc ttg ggc tcc agc   437
265 Ser Ser Pro Pro Val Leu Cys Ser Asn Ser Ser Ser Leu Gly Ser Ser
266 120             125             130                 135
268 acc ccg act ggg gcc gcg tgc gcg ccg ggg gac tac ggc cgc cag gca   485
269 Thr Pro Thr Gly Ala Ala Cys Ala Pro Gly Asp Tyr Gly Arg Gln Ala
270           140             145                 150
272 ctg tca cct gcg gag gcg gag aag cga agc ggc ggc aag agg aaa agc   533
273 Leu Ser Pro Ala Glu Ala Glu Lys Arg Ser Gly Gly Lys Arg Lys Ser
274           155             160                 165
276 gac agc tca gac tcc cag gaa gga aat tac aag tca gaa gtc aac agc   581
277 Asp Ser Ser Asp Ser Gln Glu Gly Asn Tyr Lys Ser Glu Val Asn Ser
278           170             175                 180
280 aaa ccc agg aaa gaa agg aca gca ttt acc aaa gag caa atc aga gaa   629
281 Lys Pro Arg Lys Glu Arg Thr Ala Phe Thr Lys Glu Gln Ile Arg Glu
```

```
282      185                   190                   195
284 ctt gaa gca gaa ttt gcc cat cat aat tat ctc acc aga ctg agg cga    677
285 Leu Glu Ala Glu Phe Ala His His Asn Tyr Leu Thr Arg Leu Arg Arg
286 200                   205                   210                   215
288 tac gag ata gca gtg aat ctg gat ctc act gaa aga cag gta aaa gtc    725
289 Tyr Glu Ile Ala Val Asn Leu Asp Leu Thr Glu Arg Gln Val Lys Val
290                       220                   225                   230
292 tgg ttc caa aac agg cgg atg aag tgg aag agg gta aag ggt gga cag    773
293 Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Arg Val Lys Gly Gly Gln
294              235                   240                   245
296 caa gga gct gcg gct cgg gaa aag gaa ctg gtg aat gtg aaa aag gga    821
297 Gln Gly Ala Ala Ala Arg Glu Lys Glu Leu Val Asn Val Lys Lys Gly
298          250                   255                   260
300 aca ctt ctc cca tca gag ctg tcg gga att ggt gca gcc acc ctc cag    869
301 Thr Leu Leu Pro Ser Glu Leu Ser Gly Ile Gly Ala Ala Thr Leu Gln
302      265                   270                   275
304 caa aca ggg gac tct ata gca aat gaa gac agt cac gac agt gac cac    917
305 Gln Thr Gly Asp Ser Ile Ala Asn Glu Asp Ser His Asp Ser Asp His
306 280                   285                   290                   295
308 agc tca gag cac gcc cac ctc tga                                    941
309 Ser Ser Glu His Ala His Leu
310                       300
313 <210> SEQ ID NO: 4
314 <211> LENGTH: 302
315 <212> TYPE: PRT
316 <213> ORGANISM: Homo sapiens
318 <400> SEQUENCE: 4
319 Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser Pro His Ala Thr Ala
320   1               5                   10                  15
322 Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu Ala Leu His Gly Arg
323              20                   25                   30
325 Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr Ser Ser Ser Ser Cys
326          35                   40                   45
328 Ile Ile Ala Gly Tyr Pro Asn Glu Glu Asp Met Phe Ala Ser Gln His
329      50                   55                   60
331 His Arg Gly His His His His His His His His His His Gln Gln
332 65                   70                   75                   80
334 Gln Gln His Gln Ala Leu Gln Thr Asn Trp His Leu Pro Gln Met Ser
335              85                   90                   95
337 Ser Pro Pro Ser Ala Ala Arg His Ser Leu Cys Leu Gln Pro Asp Ser
338          100                  105                  110
340 Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro Pro Val Leu Cys Ser Asn
341      115                  120                  125
343 Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr Gly Ala Ala Cys Ala Pro
344      130                  135                  140
346 Gly Asp Tyr Gly Arg Gln Ala Leu Ser Pro Ala Glu Ala Glu Lys Arg
347 145                  150                  155                  160
349 Ser Gly Gly Lys Arg Lys Ser Asp Ser Ser Asp Ser Gln Glu Gly Asn
350              165                  170                  175
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 09/16/2004
PATENT APPLICATION: US/09/940,673B   TIME: 11:44:06

Input Set : A:\22311040.app
Output Set: N:\CRF4\09162004\I940673B.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 6,21,24
Seq#:6; N Pos. 4,10

VERIFICATION SUMMARY   DATE: 09/16/2004
PATENT APPLICATION: **US/09/940,673B**   TIME: 11:44:06

Input Set : **A:\22311040.app**
Output Set: **N:\CRF4\09162004\I940673B.raw**

L:403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0